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OM nucleic - nucleic search, using sw model

Run on: October 13, 1999, 14:43:47 : Search time 2579.19 Seconds  
(without alignments)  
11986.627 Million cell updates/sec

Title: US-09-247-874-2  
Perfect score: 9721  
Sequence: 1 aagaagaagaagaagaaga.....ccgttgcctgcagtcgac 9721

Scoring table: IDENTITY\_NUC

Searched: 679419 seqs, 1590154680 residues

base :

GenEmbl: \*  
1: gb\_ba1: \*  
2: gb\_ba2: \*  
3: gb\_om: \*  
4: gb\_ov: \*  
5: gb\_pat: \*  
6: gb\_ph: \*  
7: gb\_pl1: \*  
8: gb\_pl2: \*  
9: gb\_pr1: \*  
10: gb\_pr2: \*  
11: gb\_pr3: \*  
12: gb\_ro: \*  
13: gb\_st: \*  
14: gb\_sts: \*  
15: gb\_sy: \*  
16: gb\_un: \*  
17: gb\_vl: \*  
18: em\_fun: \*  
19: em\_hlg: \*  
20: em\_hum1: \*  
21: em\_hum2: \*  
22: em\_lo: \*  
23: em\_om: \*  
24: em\_or: \*  
25: em\_ov: \*  
26: em\_pat: \*  
27: em\_ph: \*  
28: em\_pl: \*  
29: em\_ro: \*  
30: em\_sts: \*  
31: em\_sy: \*  
32: em\_un: \*  
33: em\_vl: \*  
34: gb\_hlg1: \*  
35: gb\_hlg2: \*  
36: gb\_hlg3: \*  
37: gb\_in2: \*  
38: em\_ba1: \*  
39: em\_ba2: \*  
40: em\_hum3: \*  
41: em\_hum4: \*  
42: gb\_pr4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	9717.4	100.0	9721	10	HSILB	X04500 Human gene

2	7208.8	74.2	7824	9	HUMILB	M15840 Human inter
3	1688.2	17.4	1773	5	A01613	A01613 DNA sequenc
4	1107.4	11.4	8760	3	SSPINB	X74568 S. scrofa ge
5	807.6	8.3	1473	10	HSPROIB	X56087 Human mRNA
6	807.4	8.3	1497	5	E06734	E06734 DNA encodi
7	807.4	8.3	1497	5	HOMILB	M15330 Human inter
8	788.6	8.1	1507	5	E00846	E00846 CDNA sequen
9	788.6	8.1	1507	5	I07942	I07942 Sequence 1
10	780.8	8.0	1496	9	HUMIL1	K02770 Human monoc
11	769.8	7.9	1514	5	I00729	I00729 Sequence 2
12	766	7.9	1496	9	HOMILIC	M54933 Human monoc
13	764.8	7.9	1404	5	A21148	A21148 pGIF- alpha
14	764.8	7.9	1404	5	E01230	E01230 CDNA encodi
15	764.8	7.9	1404	26	E11934	E11934 CDNA encodi
16	764.8	7.9	1404	26	E12090	E12090 Human CDNA
17	764.4	7.9	1404	5	I00228	I00228 Sequence 2
18	756.4	7.8	1469	5	I01156	I01156 Sequence 1
19	637.2	6.6	1458	5	E02498	E02498 CDNA encodi
20	612.4	6.3	614	14	G10509	G10509 human SFS C
21	573.2	5.9	7100	12	MMILIB	X04964 Murine inte
22	553	5.7	553	10	HSPROINB	X52430 H. sapiens D
23	457.6	4.7	1124	10	HSILIB	X02532 Human mRNA
24	445.6	4.6	1125	5	E00619	E00619 CDNA encodi
25	423.2	4.4	776	15	SYNLIBA	M15534 Synthetic h
26	400	4.1	400	14	G13631	G13631 human SFS S
27	395	4.1	395	10	HSPROINS7	X52431 H. sapiens D
28	379.6	3.9	1473	3	EC092481	U92481 Equus cabal
29	360	3.7	1458	3	P16PILKNLB	M86725 Sus scrofa
30	331.2	3.4	594	5	E01445	E01445 Decombinant
31	331.2	3.4	1429	5	A19155	A19155 ovine IL-1
32	325.8	3.4	1895	3	AF026543	AF026543 Bos tauru
33	307.4	3.2	986	5	E01591	E01591 CDNA encodi
34	293.4	3.0	1736	3	BOVILIB	M37211 Bovine inte
35	293.4	3.0	1750	5	I03510	I03510 Sequence 1
36	260.6	2.7	502	11	AF043335	AF043335 Homo sapi
37	251.2	2.6	141851	10	HSB75N13	Z82216 Human DNA s
38	250.2	2.6	43748	10	HSB75N13	Z82178 Human DNA s
39	250.2	2.6	136298	34	HS796117	AL035398 Homo sapi
40	249.4	2.6	133060	35	AC006474	AC006474 Homo sapi
41	249.4	2.6	162556	42	AC006017	AC006017 Homo sapi
42	249.2	2.6	131070	11	AC005295	AC005295 Homo sapi
43	248	2.6	149554	10	HSAC000111	AC000111 Human BAC
44	248	2.6	1437	12	AF119622	AF119622 Cavia por
45	247.6	2.5	130988	9	HS364122	AL031012 Human DNA

## ALIGNMENTS

RESULT	1	HSILB	9721 bp	DNA	PRI	26-JUN-1997
LOCUS	HSILB					
DEFINITION	Human gene for prointerleukin 1 beta.					
ACCESSION	X04500					
NID	933788					
VERSION	X04500.1	GI:33788				
KEYWORDS	interleukin 1 beta.					
SOURCE	human.					
ORGANISM	Homo sapiens					

REFERENCE  
1 (bases 1 to 9721)  
Primates; Catarrhini; Hominiidae; Homo.

AUTHORS  
Clark, B.D., Collins, K.L., Gandy, M.S., Webb, A.C. and Aueron, P.E.

TITLE  
Genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene

JOURNAL  
Nucleic Acids Res. 14 (20), 7897-7914 (1986)

MEDLINE  
Erratum: [[published erratum appears in Nucleic Acids Res 1987 Jan 26;15(2):868]]

COMMENT  
Data kindly reviewed (13-MAY-1988) by Clark B.D.  
FEATURES  
Location/Qualifiers  
1..9721  
/organism="Homo sapiens"



QY	1861	aacgagaaattcttcagctctctactctctgcgtcttggaaagctataaaaaagcgagga	1920
Db	1861	AACGAGAAATTCTCGACCTCTACTCTCGCTTTGAAAGCTATAAACGACGAGGA	1920
QY	1921	gaactgcgaatcccaactctctcgaagcaaaagcaaacagctcctctggatcc	1980
Db	1921	GAAACTGCGAATCCCAACTCTCTGAGGACAAAGGCACAAAGGCTCTCTGGGATTC	1980
QY	1981	tcttcagccaattcttcattctgcgaaglatgaacttaattcttccttaacaactagtgctaa	2040
Db	1981	TCTTCAGCAATCTTCAATGCTGTCAGATGACTTATCTCTTCAACCTAGGTGTAA	2040
QY	2041	gggagctctctctgctctctctgcctctcttggtgtatagcatatctctctctctct	2100
Db	2041	GGGAGCTCTCTGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2100
QY	2101	tcttcaagccttttgcaaaaag	2160
Db	2101	TCTTCT	2160
QY	2161	ccaggctgaataataigtcttatagctcgggaaaatacttcgggaatgtaactgcttatct	2220
Db	2161	COAGGTGAATAATAGCTTATGACGTGGGAATATTCTGGAATGATAGCTGTTATCT	2220
QY	2221	aacagctgaacccctaaaggtatgctcaagcctctctgcagcctctctcagccaatc	2280
Db	2221	AACAGCTGACCCCTAAAGGTATTGTCAAAGCCTCTGCTCCAGCTCTCTGCGCAATAC	2280
QY	2281	attgttagttgggtttgggttttagcaagtctttctctcagaccaaaagaactctctt	2340
Db	2281	ATTGTTAGTTGGGTTGGGTTTAGCAAAATCCTTTTCTCTAGACCCAAAGGACTCTCTTT	2340
QY	2341	cacacattcatctattactcagaagatcaattctcttgatcagctcgaactgagatgc	2400
Db	2341	CACACATTCAATTCATTACTGAGAGATCATTTCTTGCAAGACTGCGACATGATGTC	2400
QY	2401	tgaaggaataccacacatgagacgtagccgctcagtgagggaagtcactcaattctctcttta	2460
Db	2401	TGAGGAATACACACATGAAGAGTGGCGGTATGGGGAAGACATCTATTTCCTCTTTTA	2460
QY	2461	cacaggtctctgaaagcagccctgagcaaaagtactgagctcgcgcaatgaaatgagctt	2520
Db	2461	CACAGGTCTCTGAAAGCACCCATGGACAAAGTACTGAGCTCGCCAGTGAATGATGTGCTT	2520
QY	2521	attacaagctcagtgagagacgtctgagcaagaaatcagatcaggtctctctctcaagat	2580
Db	2521	ATTAAAGCTCAGTGGAGACGCTGAGACCAAGTAATAGCAGGCTCTCTTTCAAGAT	2580
QY	2581	agagtgatcatctgctgtgtgagaccagaatlttcccctaattgtccctcttcagtgcaa	2640
Db	2581	AGAGTGATCTGCTGCTGTGGAGACAGATTTTTTCCCTAAATGGCTCTTTCAGTGGCAA	2640
QY	2641	acaaggtgcgaagtcaaatctgatttaaagactacttcccatacaagtcctcccaagct	2700
Db	2641	ACAGGTTGTCCAAGTAAATCTGATTTAAAGACTACTTTCCTATTAACAAGTCCCTCCAGCT	2700
QY	2701	tggagccctggagagctatccagaatggtgttgagcaaggtctccctcgaaagcaaatg99g	2760
Db	2701	TGGAGCCTGGAGAGCTATCCAAATGTGTGTTGTCGAAGGCTCTCTCGACAGAGCAAAATG99G	2760
QY	2761	agaaaaagatltccaaagccacatacaagaalccccttgcanaagtgtygcttfgaag9ag	2820
Db	2761	AGAAAAAGATTCCAAGCCCAATACAAAGGAATCCCTTTCGAAAGTGTCGCTTGAGAGGAG	2820
QY	2821	agggagagctcaagatttaagctgactctgctgggcttagaggttaagctcaaatcccaac	2880
Db	2821	AGGGAGAGCTCAGATTTTAGTGACTCTGCTGGGCTTAGAGGTTAAGGCTCAAGATCCAAC	2880
QY	2881	agggagaccaaagtgycacactgcacagccttaaatctgactctgagctgtctcgagc	2940
Db	2881	AGGGAGCACAAAGGTGCCACCTTGCCAGGCTACAAATCTGCTTCTTGAGATGTTCTGCGC	2940

QY	2941	atatacagtgaaactctggccaaggtgtttcaaggaagctttgaaggcaagctgttgcagt	3000
Db	2941	ATATACACTGTAAACTCTGCCAGAGTGTTCAGGAGCTTTGAGAGCGAGGCTGTGTTCAGT	3000
QY	3001	ttcttatgaacaagcaagctctgtacaaaggaaggaaaaataaacctcttttagaagca	3060
Db	3001	TTCTTATGAAACAGTCAAGCTGTGTACACAGGAGGAAAAATTAACCTGTTTAGAAGCA	3060
QY	3061	taattgagaaatgtccctgttttattacagtgagcaatgaggatgactgttctttgaag	3120
Db	3061	TAATTGAGAACTGTCCCTGTTTATATACAGTGGCAATGAGATGACTGTTCTTTGAAG	3120
QY	3121	ctgtagggccccaacaacagaataagtaagactatagggttaactcccaacccaagaagag	3180
Db	3121	CTGATGGCCCTAACAAGCTAAGTAAGATAGGAGTTAGGTTAACTCCCAACCCAAGGAAGG	3180
QY	3181	ctctaacacaaggaagaactctaaagaaggaagtctctggccaacttgatgccatgtactt	3240
Db	3181	CTCTAACACAAGGGAAGACTCTAAAGAAGGAGTTCTGTGGCACTTTGATGCCATGTTATT	3240
QY	3241	tgatttgaagaagacttaacccctcccaagtgagacaagagctgcaccaactgtgacctg	3300
Db	3241	TGATTTGAAGAAGACTTTAACTTCCCTCCAGTAGACACACAGGCTGCACCACTTCTGACCTG	3300
QY	3301	ggcaacttggatcatatatacccaagctgactcccaactaagctgtgtgtgtgtggccaactt	3360
Db	3301	GGCACTTGGATCATATATCCACACAGTCACTCACTAAGCTTGGTGTGTGTGGCCCACTT	3360
QY	3361	ggttgtagcaagggagagagtagtgataaagtcccaattccatagtagaagaacaacaaag	3420
Db	3361	GGTGTGACAGGGGAGGAGTAGTAGTAAATGTTCCCTTCATAGTAGAGAACAAACCAAG	3420
QY	3421	tcttcacaataaalttgatataccctcttlaagagatgattacacgtacataatgccaactctg	3480
Db	3421	TCTTCACAATAAATTTGATATATCTTTTAAAGATGATGATTCAGCTTACCTTAAGCCATACCTG	3480
QY	3481	agttaaactctgaaacccaagaagatgtactcttgagaactaataatgtctaacccctttgag	3540
Db	3481	AGTTAAACTCTGAAACCCAAAGATGATCTTTGAACATAATGCTACCCCTTTGAG	3540
QY	3541	tagaatagttttctgcaacttgagggtggaagctatacaaaagaagcatagatgatataaa	3600
Db	3541	TAGAATAGTTTCTTGCACTGCTGGGGTGAACCTTATACAAACAAGCATAGATGATATAA	3600
QY	3601	caaaaagaatgaaatgaaacttgaagaagaaacacatcacttctgtctgttacccttgaagaat	3660
Db	3601	CAAAAAGATGAATGAAACTTGAAGAAACCAACATCACTGCTGTGACCTTGACAGT	3660
QY	3661	catttccccgcttttgaaactatctgcgaaaataaaggctgagctgtaagatctctgag	3720
Db	3661	CATTTTCCCGCTTTGAACTCATCTGAAATAAAGGGCTAGCTGATGATCTCTGAG	3720
QY	3721	attccagatcccttgcgaacccctcagctctcgaatatcttaagctgtagtaaggagcatgtg	3780
Db	3721	ATTCCAGATCCCTGCCAACCTCCAGTCTGAAATATTTTAGTTAGCTTAAGGECATTTG	3780
QY	3781	ggcagcaaatggtatcatttccagatccatccctacaaagagcaatgtatataatccctgtg	3840
Db	3781	GGCAGCAAAATGGTCACTTTTCCAGCATCATCTTACAAAGACCATGTATATTCCTGTG	3840
QY	3841	tcctcttctgtttatataagatgcacagtagacttctcaggtgtccagacatcaagctagct	3900
Db	3841	TCCTCTTCTGTTTATATAGATGCTCACTACACTTCTCAGGTGTCCAGCATACAGCTACT	3900
QY	3901	aggcagactgtgcaaggtttgagagcagcaacttctctcgtgcttattttatccagtttg	3960
Db	3901	AGGCACATTGTGCAGGTTGAGAGGCACCACTTTCTCTGCTTTATTTTATTCACAGTTG	3960
QY	3961	tgaatagctcccccagcctcatataatccagttccctcaactctgtttaaaaaacatatctctta	4020
Db	3961	TGAATAGCTCCCCAGCCTCATATATCCAGTCTCAATCTGTATAAAAAATATTTCTTTA	4020
QY	4080	attttaagactgcgataaactctcttgcctgcagctgtggaagagccatctgagctgt	4080

Db	4021	GAAGTTTAAACAGCGCATACCTTCTTGCGTGGAGGTGGAGAGGCCATTTGGCTTGT	4080
Oy	4081	ctgccttgcccttgcgcccccattgcgcctctccagcagcttggtctgcgtccagagaa	4140
Db	4081	CTGCGTGGCCTTTCGCCCCCATTCGCTTCCAGCAGCTGGGTCTGCTCCAGCGAGAA	4140
Oy	4141	attctctctgcctcaacttctcttctgtgcactacagctctcttaactgcttccaagc	4200
Db	4141	ATTCTCTCTCTCAACTTTCTTTCTTGGCACTTACAGGTCCTTTTAAGTGTTCAMGC	4200
Oy	4201	cttgcgaacattatcagcgccttaagcgaacctcagtgaaaccttaacgagctctctg	4260
Db	4201	CTTGGAAACCATTAACACCTTAAGGCAMCCTCAGTCAACCCCTTAATACGACCTTCTCG	4260
Oy	4261	aataagaggaagagtggtgacaattccacaanaagctactccacagatttgcaagtctc	4320
Db	4261	AATAAGAGGAAGAGTGGTGAACATTTCCACMAAATACTCTCCACAGGATTGGCAAGTGGCT	4320
Oy	4321	atgcagacagtgctta.tgcaaaaaaggaaaaaaagacagtgtagaaaattgca.tactgct	4380
Db	4321	ATGACAGAGTGTATGAAAAAGGAAAAAAGAACAGTGTACAAAAATTGAAATACTTCT	4380
Oy	4381	gaatgcagcatatggtgaaatgtaaaatgctatgctatcgtcatcgtgaaagcaaatcatagt	4440
Db	4381	GAGTGAAGCATATGGTGAAATGGAAAAATGTTATGTCATCTGCATGAIAAAAGCAATCATAGT	4440
Oy	4441	gtgcgaacatttaaggaatacaaaaaagatatagaanaagctataatgtataggttagtggtg	4500
Db	4441	GTGCACAGCATTTAGGATATACAAAAAGATATAGCAAAAGTATACATGTATAGTGTAGTGGG	4500
Oy	4501	gcattgtaaaaaaagatgacaaagttagaatcggaattatcttaagaataagccgtgaagt	4560
Db	4501	GCATGTACAAAAAGATATACAAAGTAAATGGAGTTATCTTAAGATATAGCTGTAAAGT	4560
Oy	4561	gtccagaagccaaatctctagcttgagctgcgcctcctacccgtgtgtgccttgatga	4620
Db	4561	GTCGAGAGCCACATTTGACTTTGAGTGGCTGACCTACTGCTGTTGTGGCTTAGTACA	4620
Oy	4621	gccctaacctccctgagcctccagaagggataatccttlatattatattatctatctt	4680
Db	4621	CCCTTAACCTCTCTGACCTTCCACAGAGGGATATCTTTATTTATTTATTTATTTATTT	4680
Oy	4681	gttttgatttgattgtctgtcttcttcttaagacagagctcactcctgttgccagagctga	4740
Db	4681	GTTTGTGTTTGTGTTTGTGTTGTTTATGAGACAGAGTCACTCTGTGTGCCAGGCTTGA	4740
Oy	4741	gtgcagtggtacaatcctgtgcttaactgcatcctccactcctcagttcaagcgattctc	4800
Db	4741	GTCGAGTGTACATCTTTGGCTTACTGTCATCTCCACCTCTGAGTCAAGGATTTGCC	4800
Oy	4801	ttctctagctccctcgatlaagcttagattaaaggtgtaaccaaccacacacccagctaat	4860
Db	4801	TTCTCTAGCTCCCTCGAATTAAGTATACGTATACAGGTGACCCCAACACCCACAGCTAATTT	4860
Oy	4861	tgatcttcttagtagaagaagggtctgcacatgttgccagagcttggtttgaagctctcag	4920
Db	4861	TGATTTTCTTAGTAGAAGAGGGGTTTGCCATGTGGCCAGGCTGGTTTGAAGTCTTAC	4920
Oy	4921	ctaaagattcaatccacactcgcctcccaaaagtctggaattacagagcatgaagccacac	4980
Db	4921	CTAAATGATTCATCCACCTCGGCTTCCCAAAAGTGTGGATTACAGGATGAGCCACAC	4980
Oy	4981	gccctgcgccagagagagatgatctctttagaagctcgggaattcttcaagccttccctc	5040
Db	4981	GCCCTGCCCCAGAGGGGATATCTTTTGAAGCTCCGGGATCTTTTAAAGCCCTTCTCTCT	5040
Oy	5041	ctctgagcttctcactcctcgtatcacaagcatggtctcttgccagagcactcactcagg	5100
Db	5041	CTCTGAGCTTCTACTCTCTGATGTCAAAAGCATGTTCTCTGCCAGAGCACCTCACAGG	5100
Oy	5101	ctctccctctgctctctcccgagtgctctcttccagagcactgaaacctctgcctctgat	5160

QY	6241	ccctgagaataatgacggcctcaagacacactccaccagacatgtccaccacccaagtctcttgggca	6300
Db	6241	cctgagaaattatgacggcctcaagacacactccaccagacatgtccaccacccaagtctcttgggca	6300
QY	6301	tagtgcagtgatcaattcttccacaataatggggtcatcttgatggaatgagccctaactgct	6360
Db	6301	tagtgcagtgatcaattcttccacaataatggggtcatcttgatggaatgagccctaactgct	6360
QY	6361	gtgggtctctctctctctgtgtgtgtgaggtgcgaacaagatgctggaagcgaataatgtgtcc	6420
Db	6361	gtgggtctctctctctctctgtgtgtgtgaggtgcgaacaagatgctggaagcgaataatgtgtcc	6420
QY	6421	atccccctcccaagtccttccccccttggcccacaactccgtccacccaatgccaagtgtgt	6480
Db	6421	atccccctcccaagtccttccccccttggcccacaactccgtccacccaatgccaagtgtgt	6480
QY	6481	tccctgtgaaggaaatttaccgcccagaagaactatatactctccgctgtgaaggagca	6540
Db	6481	tccctgtgaaggaaatttaccgcccagaagaactatatactctccgctgtgaaggagca	6540
QY	6541	aaatttcaagtgtcggtgtgaaccatcaatagctgtgtgatatgctgtgaaatcgatcgccaca	6600
Db	6541	aaatttcaagtgtcggtgtgaaccatcaatagctgtgtgatatgctgtgaaatcgatcgccaca	6600
QY	6601	gtagccaagaagcctctgcacagagagtggtggtgaactaaaggctgtcgttaatttgaaggacag	6660
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QY	6661	ctcaactcagggggaagcatttggctctccacagccagagccaagaataactcgttcttggaa	6720
Db	6661	ctcaactcagggggaagcatttggctctccacagccagagccaagaataactcgttcttggaa	6720
QY	6721	tcgggttagtaagatgtatcccaagggcctccaatgtgaacacgcgtgtacatggaagaatca	6780
Db	6721	tcgggttagtaagatgtatcccaagggcctccaatgtgaacacgcgtgtacatggaagaatca	6780
QY	6781	aaatgagtgctctctcttggagccacttcccaagcccaagctctctctcccaagttctt	6840
Db	6781	aaatgagtgctctctcttggagccacttcccaagcccaagctctctctcccaagttctt	6840
QY	6841	cccaatgggccaactctcgttccctggaacaagttctgtgtcgtatcttctgacagaatgaca	6900
Db	6841	cccaatgggccaactctcgttccctggaacaagttctgtgtcgtatcttctgacagaatgaca	6900
QY	6901	gctcaacctcttcccttcttccatcccaattgatacaagttgttcgcctctgtgagatggca	6960
Db	6901	gcttccacctcttcccttcttccatcccaattgatacaagttgttcgcctctgtgagatggca	6960
QY	6961	catggcagccagatgacacaatgtgtcttcccttcccttcccttccgaatttaaaatgtag	7020
Db	6961	catggcagccagatgacacaatgtgtcttcccttcccttcccttccgaatttaaaatgtag	7020
QY	7021	aaccttcttcaatctcgttcttccatgtatagagctctggaacaacctgaagccttga	7080
Db	7021	aaccttcttcaatctcgttcttccatgtatagagctctggaacaacctgaagccttga	7080
QY	7081	ggggaacaacctaaatcaacaataatgaacctgtcatgtctgtgagaagtcaagttatccct	7140
Db	7081	ggggaacaacctaaatcaacaataatgaacctgtcatgtctgtgagaagtcaagttatccct	7140
QY	7141	gtgtcttaagccaagaacctcaactgtgtgtgttcccaagaaggtcacaattacatglatc	7200
Db	7141	gtgtcttaagccaagaacctcaactgtgtgtgttcccaagaaggtcacaattacatglatc	7200
QY	7201	ctactctcggggtcgaagggttgggtgtgaacctgtatgtctgttcccttaaccaagaacct	7260
Db	7201	ctactctcggggtcgaagggttgggtgtgaacctgtatgtctgttcccttaaccaagaacct	7260
QY	7261	cccttcttcttccagtggtgttctccatgtctcttgttcaagaaggaagaagtaatgaca	7320
Db	7261	cccttcttcttccagtggtgttctccatgtctcttgttcaagaaggaagaagtaatgaca	7320

QY 7321 aatactctgacctgagccctcaagaaagaatctgtacccgtctgctgctgctgaaga 7380  
DB 7321 AATACCTGTGGCTTGGGCTCAAGAAAAAATCTGTACCTGTCTGTGGTGTGAAGA 7380  
QY 7381 tgaataagccactctcaagcttgaaglaagtgatgctatggaatgaagccctctcaag 7440  
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QY 7441 cctctgacacactatctcccaagaatcaatcaactctcccgcccccacccctagaaga 7500  
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